FIG. 1A

```
        10                      30                      50
GAATTCGGCACGAGCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGACATCA
        70                      90                     110
ACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCCCCAA
       130                     150                     170
CCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGAGCAGTCACGCCTTAC
                        M  D  D  S  T  E  R  E  Q  S  R  L  T
       190                     210                     230
TTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACG
 S  C  L  K  K  R  E  E  M  K  L  K  E  C  V  S  I  L  P  R
       250                     270                     290
GAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCT
 K  E  S  P  S  V  R  S  S  K  D  G  K  L  L  A  A  T  L  L
       310                     330                     350
GCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCA
 L  A  L  L  S  C  C  L  T  V  V  S  F  Y  Q  V  A  A  L  Q
       370                     390                     410
AGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGC
 G  D  L  A  S  L  R  A  E  L  Q  G  H  H  A  E  K  L  P  A
       430                     450                     470
AGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAA
 G  A  G  A  P  K  A  G  L  E  E  A  P  A  V  T  A  G  L  K
       490                     510                     530
AATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG
 I  F  E  P  P  A  P  G  E  G  N  S  S  Q  N  S  R  N  K  R
       550                     570                     590
TGCCGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAG
 A  V  Q  G  P  E  E  T  V  T  Q  D  C  L  Q  L  I  A  D  S
```

FIG. 1B

```
       610                 630                 650
TGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAA
 E  T  P  T  I  Q  K  G  S  Y  T  F  V  P  W  L  L  S  F  K
       670                 690                 710
AAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTT
 R  G  S  A  L  E  E  K  E  N  K  I  L  V  K  E  T  G  Y  F
       730                 750                 770
TTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCA
 F  I  Y  G  Q  V  L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q
       790                 810                 830
GAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTAT
 R  K  K  V  H  V  F  G  D  E  L  S  L  V  T  L  F  R  C  I
       850                 870                 890
TCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAAACT
 Q  N  M  P  E  T  L  P  N  N  S  C  Y  S  A  G  I  A  K  L
       910                 930                 950
GGAAGAAGGAGATGAACTCCAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGA
 E  E  G  D  E  L  Q  L  A  I  P  R  E  N  A  Q  I  S  L  D
       970                 990                1010
TGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGT
 G  D  V  T  F  F  G  A  L  K  L  L
      1030                1050                1070
AGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAA
      1090                1110                1130
AAAAAAAAAAAAAAAAAAAAAAAAAGTAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
      1150                1170
AAAAAAAAAAAAAAAAAAAAAACTCGGAGGGGG
```

FIG. 2A

```
        10                          30                          50
GAATTCGGCACGAGCTCCAAAGGCCTAGACCTTCAAAGTGCTCCTCGTGGAATGGATGAG
                                                         M  D  E
        70                          90                          110
TCTGCAAAGACCCTGCCACCACCGTGCCTCTGTTTTTGCTCCGAGAAAGGAGAAGATATG
S  A  K  T  L  P  P  P  C  L  C  F  C  S  E  K  G  E  D  M
        130                         150                         170
AAAGTGGGATATGATCCCATCACTCCGCAGAAGGAGGAGGGTGCCTGGTTTGGGATCTGC
K  V  G  Y  D  P  I  T  P  Q  K  E  E  G  A  W  F  G  I  C
        190                         210                         230
AGGGATGGAAGGCTGCTGGCTGCTACCCTCCTGCTGGCCCTGTTGTCCAGCAGTTTCACA
R  D  G  R  L  L  A  A  T  L  L  L  A  L  L  S  S  S  F  T
        250                         270                         290
GCGATGTCCTTGTACCAGTTGGCTGCCTTGCAAGCAGACCTGATGAACCTGCGCATGGAG
A  M  S  L  Y  Q  L  A  A  L  Q  A  D  L  M  N  L  R  M  E
        310                         330                         350
CTGCAGAGCTACCGAGGTTCAGCAACACCAGCCGCCGCGGGTGCTCCAGAGTTGACCGCT
L  Q  S  Y  R  G  S  A  T  P  A  A  A  G  A  P  E  L  T  A
        370                         390                         410
GGAGTCAAACTCCTGACACCGGCAGCTCCTCGACCCCACAACTCCAGCCGCGGCCACAGG
G  V  K  L  L  T  P  A  A  P  R  P  H  N  S  S  R  G  H  R
        430                         450                         470
AACAGACGCGCTTTCCAGGGACCAGAGGAAACAGAACAAGATGTAGACCTCTCAGCTCCT
N  R  R  A  F  Q  G  P  E  E  T  E  Q  D  V  D  L  S  A  P
        490                         510                         530
CCTGCACCATGCCTGCCTGGATGCCGCCATTCTCAACATGATGATAATGGAATGAACCTC
P  A  P  C  L  P  G  C  R  H  S  Q  H  D  D  N  G  M  N  L
        550                         570                         590
AGAAACATCATTCAAGACTGTCTGCAGCTGATTGCAGACAGCGACACGCCGACTATACGA
R  N  I  I  Q  D  C  L  Q  L  I  A  D  S  D  T  P  T  I  R
```

FIG. 2B

```
       610                  630                  650
AAAGGAACTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGAGGAAATGCCTTGGAG
K  G  T  Y  T  F  V  P  W  L  L  S  F  K  R  G  N  A  L  E
       670                  690                  710
GAGAAAGAGAACAAAATAGTGGTGAGGCAAACAGGCTATTTCTTCATCTACAGCCAGGTT
E  K  E  N  K  I  V  V  R  Q  T  G  Y  F  F  I  Y  S  Q  V
       730                  750                  770
CTATACACGGACCCCATCTTTGCTATGGGTCATGTCATCCAGAGGAAGAAAGTACACGTC
L  Y  T  D  P  I  F  A  M  G  H  V  I  Q  R  K  K  V  H  V
       790                  810                  830
TTTGGGGACGAGCTGAGCCTGGTGACCCTGTTCCGATGTATTCAGAATATGCCCAAAACA
F  G  D  E  L  S  L  V  T  L  F  R  C  I  Q  N  M  P  K  T
       850                  870                  890
CTGCCCAACAATTCCTGCTACTCGGCTGGCATCGCGAGGCTGGAAGAAGGAGATGAGATT
L  P  N  N  S  C  Y  S  A  G  I  A  R  L  E  E  G  D  E  I
       910                  930                  950
CAGCTTGCAATTCCTCGGGAGAATGCACAGATTTCACGCAACGGAGACGACACCTTCTTT
Q  L  A  I  P  R  E  N  A  Q  I  S  R  N  G  D  D  T  F  F
       970                  990                 1010
GGTGCCCTAAAACTGCTGTAACTCACTTGCTGGAGTGCGTGATCCCCTTCCCTCGTCTTC
G  A  L  K  L  L
      1030                 1050                 1070
TCTGTACCTCCGAGGGAGAAACAGACGACTGGAAAAACTAAAAGATGGGGAAAGCCGTCA
      1090                 1110                 1130
GCGAAAGTTTTCTCGTGACCCGTTGAATCTGATCCAAACCAGGAAATATAACAGACAGCC
      1150                 1170                 1190
```

FIG. 3A

```
       1                                                  50
Hagp3  MDDSTER.EQ SRLTSCLKKR EEMKLKECVS ILPRKESPSV RSSKDGKLLA
Magp3  MDESAKTLPP PCLCFCSEKG EDMKVGYDPI TPQKEEGAWF GICRDGRLLA
 cons  MD.S...... ..L..C..K. E.MK...... .....E.... ....DG.LLA

       51                                                100
Hagp3  ATLLLALLSC CLTVVSFYQV AALQGDLASL RAELQGHHAE KLPAGAGAPK
Magp3  ATLLLALLSS SFTAMSLYQL AALQADLMNL RMELQSYRGS ATPAAAGAPE
 cons  ATLLLALLS. ..T..S.YQ. AALQ.DL..L R.ELQ..... ..PA.AGAP.

       101                                               150
Hagp3  AGLEEAPAVT AGLKIFEPPA PGEGNSSQNS RNKRAVQGPE ET........
Magp3  ........LT AGVKLLTPAA PRPHNSSRGH RNRRAFQGPE ETEQDVDLSA
 cons  .........T AG.K...P.A P...NSS... RN.RA.QGPE ET........

       151                             B                 200
Hagp3  .......... .......... ...VTQDCLQ LIADSETPTI QKGSYTFVPW
Magp3  PPAPCLPGCR HSQHDDNGMN LRNIIQDCLQ LIADSDTPTI RKGTYTFVPW
 cons  .......... .......... .....QDCLQ LIADS.TPTI .KG.YTFVPW
```

FIG. 3B

```
       B'         C'      C         D             E        250
Hagp3  LLSFKRGSAL EEKENKILVK ETGYFFIYGQ VLYTDKTYAM GHLIQRKKVH
Magp3  LLSFKRGNAL EEKENKIVVR QTGYFFIYSQ VLYTDPIFAM GHVIQRKKVH
 cons  LLSFKRG.AL EEKENKI.V. .TGYFFIY.Q VLYTD...AM GH.IQRKKVH

       251    F                       G            H       300
Hagp3  VFGDELSLVT LFRCIQNMPE TLPNNSCYSA GIAKLEEGDE LQLAIPRENA
Magp3  VFGDELSLVT LFRCIQNMPK TLPNNSCYSA GIARLEEGDE IQLAIPRENA
 cons  VFGDELSLVT LFRCIQNMP. TLPNNSCYSA GIA.LEEGDE .QLAIPRENA

       301        I     317
Hagp3  QISLDGDVTF FGALKLL
Magp3  QISRNGDDTF FGALKLL
 cons  QIS..GD.TF FGALKLL
```

FIG. 4A

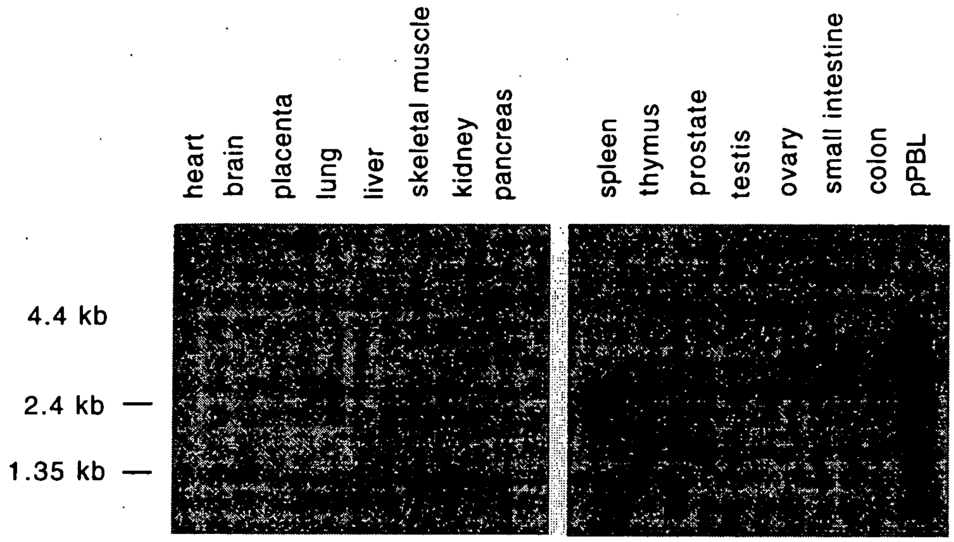

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
spleen
thymus
prostate
testis
ovary
small intestine
colon
pPBL
4.4 kb
2.4 kb
1.35 kb

FIG. 4B

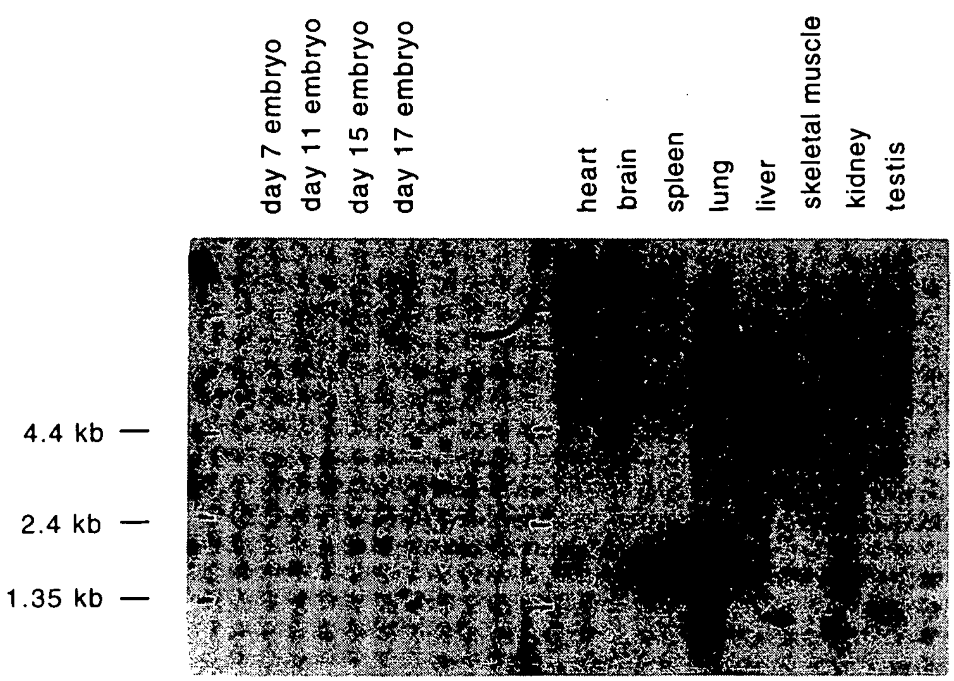

day 7 embryo
day 11 embryo
day 15 embryo
day 17 embryo
heart
brain
spleen
lung
liver
skeletal muscle
kidney
testis
4.4 kb
2.4 kb
1.35 kb

FIG. 5A

FIG. 5B

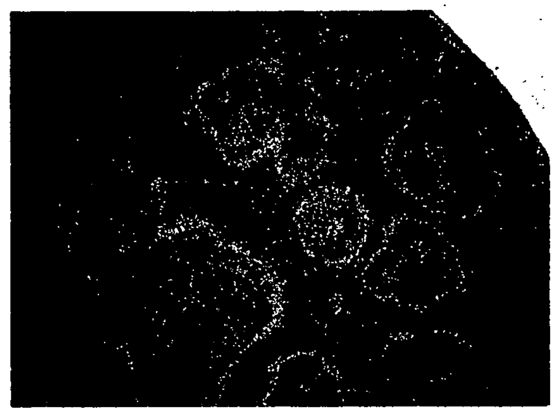


FIG. 5C

FIG. 5D

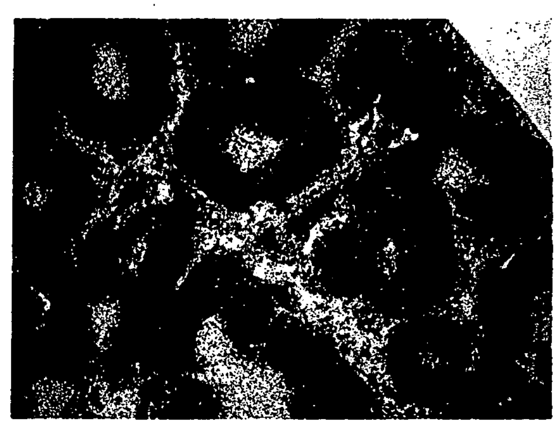


FIG. 5E

FIG. 5F

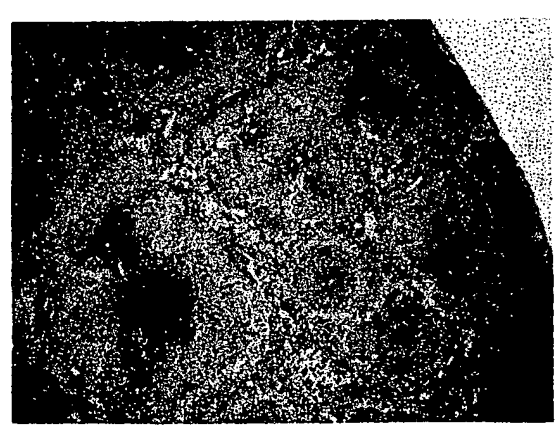


FIG. 6A

FIG. 6B

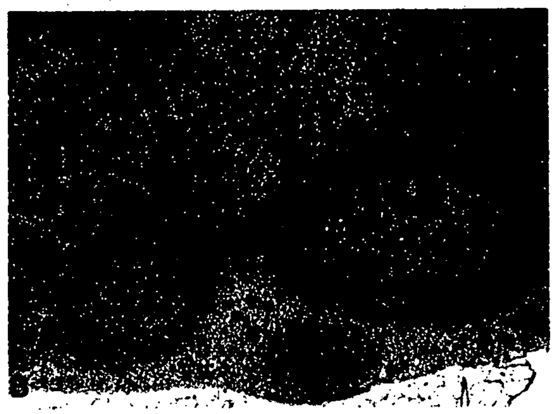


FIG. 6C

FIG. 6D

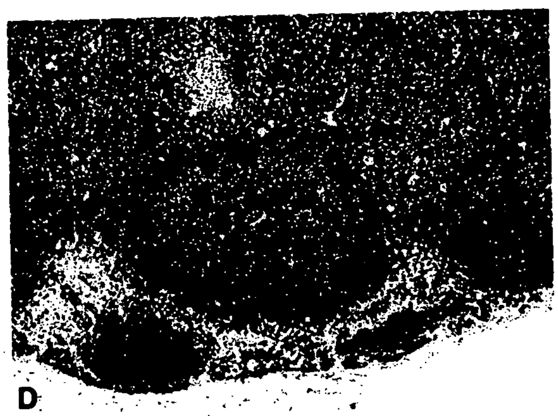


FIG. 6E

FIG. 6F

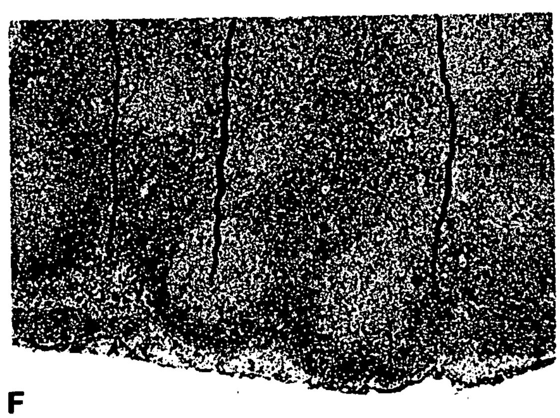


FIG. 7A

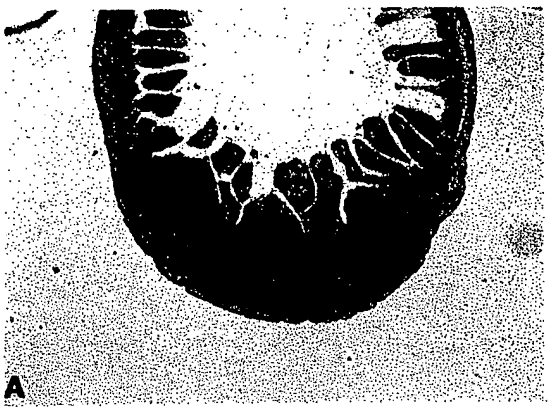


FIG. 7B

FIG. 7C

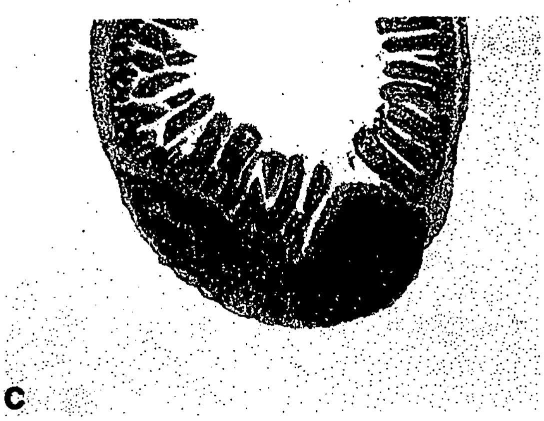


FIG. 7D

FIG. 7E

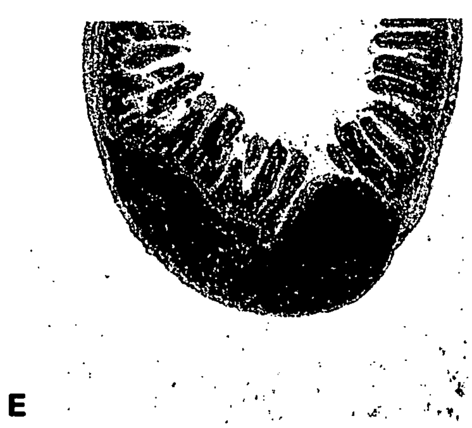


FIG. 7F

FIG. 8A

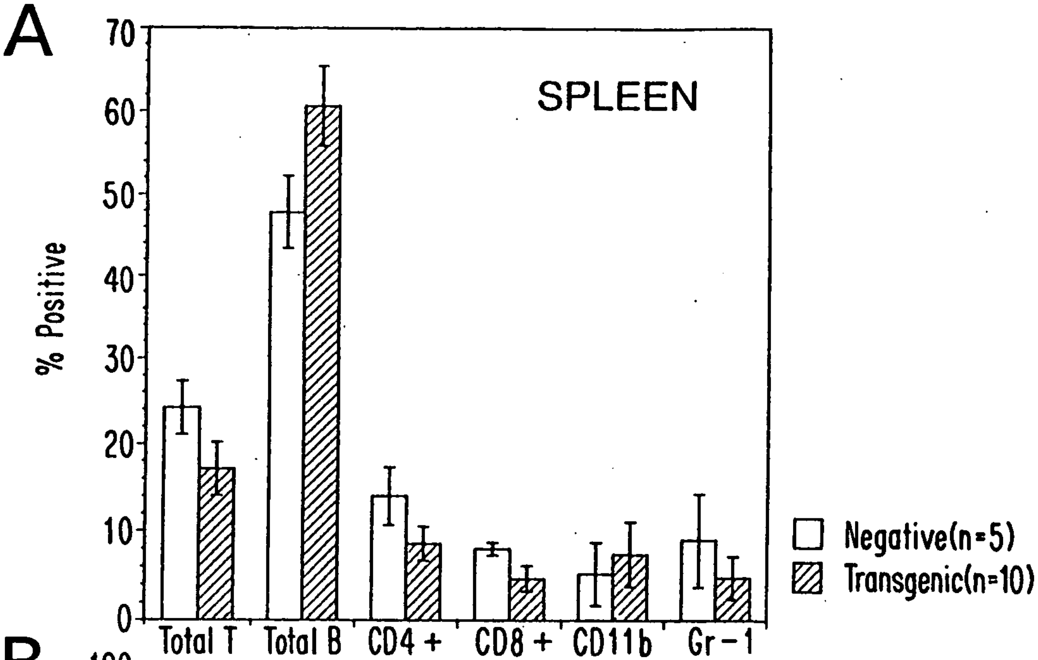


FIG. 8B

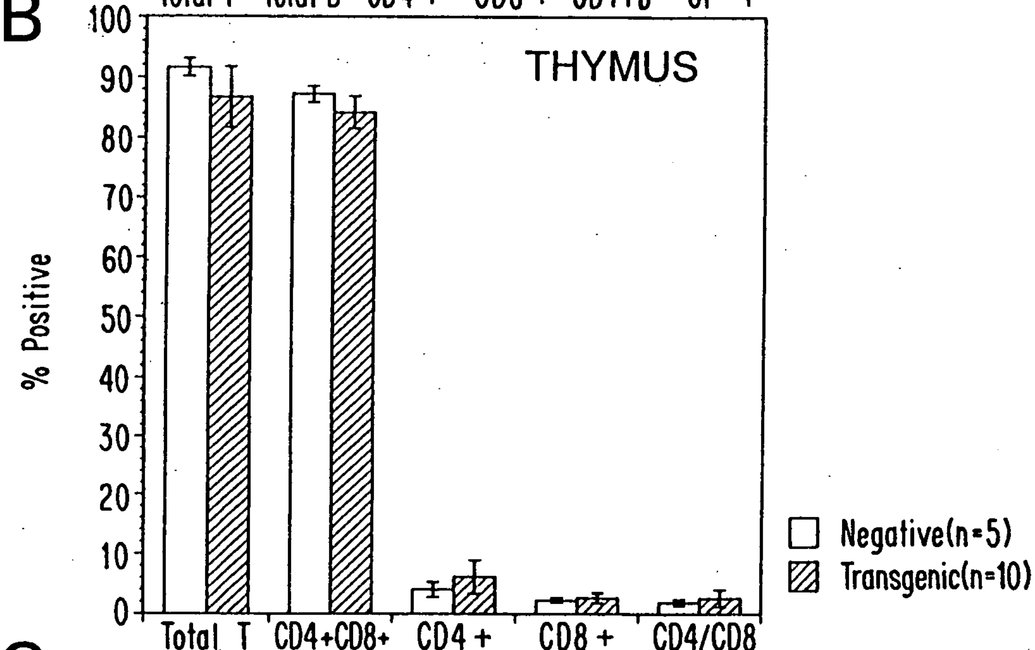


FIG. 8C

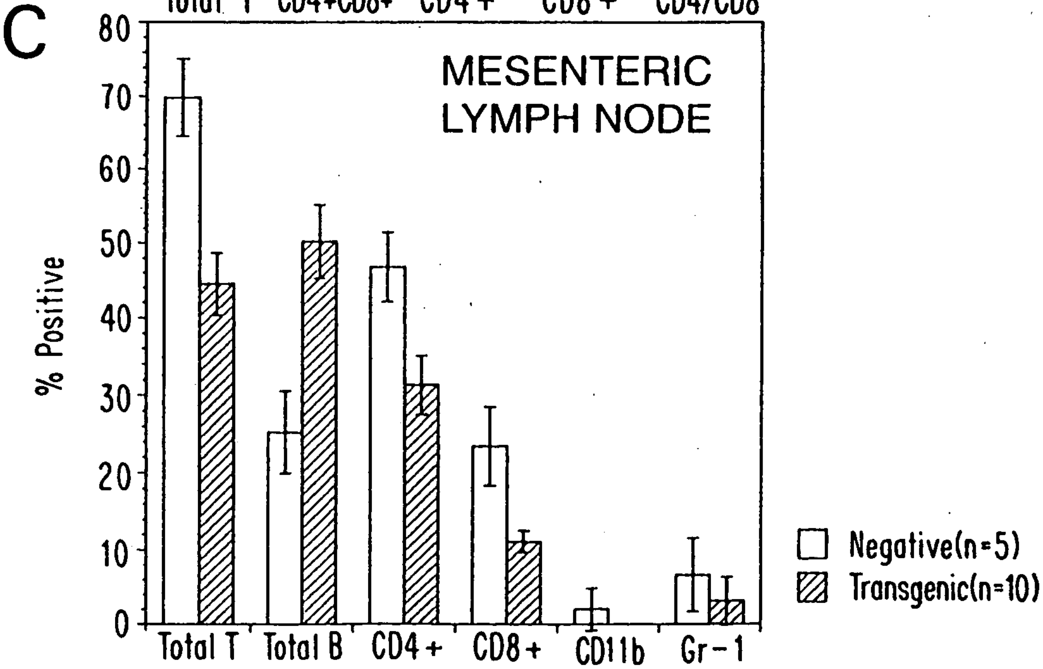


FIG. 9A

```
           B                     B/B' loop                 B'    C'      C        D         D/E loop    E
      -----+PAAHLT--P---------------------L-W--------A-LS-GV-L-N----LVV---GLYFIYSQV-F+GQ-CP-------V-L       Consensus
139-  EKKELRKVAHLTGKSN---------------SRS-MPLEWEDTYGI--VLLS-GVKYKK--GGLVINETGLYFVYSKVYFRGQSCN------NLPL       Human FasL
137-  EKKEPRSVAHLTGNPH---------------SRS-IPLEWEDTYGT--ALIS-GVKYKK--GGLVINETGLYFVYSKVYFRGQSCN------NQPL       Mouse FasL
136-  ETKKPRSVAHLTGNPR---------------SRS-IPLEWEDTYGT--ALIS-GVKYKK--GGLVINEAGLYFVYSKVYFRGQSCN------SQPL       Rat FasL
116-  GDQNPQIAAHVISEASS--------------KTT-SVLQWAEKGYY--TMSNNLVTLENG-KQLTVKRQGLYYIYAQVTFCSNREA----SSQAPF      Human CD40L
115-  GDEDPQIAAHVVSEANS--------------NAA-SVLQWAKKGYY--TMKSNLVMLENG-KQLTVKREGLYYVYTQVTFCSNREP----SSQRPF      Mouse CD40L
142-  ---VTQDCLQLIADSETPTIQ-------KGSY--TFVPWLLSFKR-GSALE---EKEN--KIL-VKETGYFFIYGQVLYT-DKT-----YAMGHL      Human AGP3
163-  LRNIIQDCLQLIADSDTPTIR-------KGTY--TFVPWLLSFKR-GNALE---EKEN--KI-VVRQTGYFFIYSQVLYT-DPI-----FAMGHV      Mouse AGP3
157-  GKPEAQPFAHLTINAASIP---------SGSHKVTLSSWYHDRGW--AKISN-MTLSNG-K-LRVNQDGFYYLYANICFRHHETS----GSVPTD      Mouse OPGL
158-  SKLEAQPFAHLTINATDIP---------SGSHKVSLSSWYHDRGW--AKISN-MTFSNG-K-LIVNQDGFYYLYANICFRHHETS----GDLATE      Human OPGL
116-  ERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH-SFLSN-LHLRNG-E-LVIHEKGFYYIYSQTYFRFQEE------IKENT      Human TRAIL
120-  GGRPQKVAAHITGITRRSNSALIPISKDGKTLGQKIESWESSRKGH-SFLNH-VLFRNG-E-LVIEQEGLYYIYSQTYFRFQEAEDASKMVSKD-      Mouse TRAIL
 92-  RAPFKKSWAYLQVAKH---------------LNK-TKLSWNKDG-----ILH-GVRYQD--GNLVIQFPGLYFIICQLQFLVQ-CP----NNSVDL      Human CD30L
 97-  STPSKKSWAYLQVSKH---------------LNN-TKLSWNEDG-----TIH-GLIYQD--GNLIVQFPGLYFIVCQLQFLVQ-CS----NHSVDL      Mouse CD30L
 82-  DLSPGLPAAHLIGAP----------------LKGQ-GLGWETTKEQ--AFLTSGTQFSDA-EGLALPQDGLYYLYCLVGYRGRAPPGGGDPQGRSV     Human LyTβ
148-  DLNPELPAAHLIGAW----------------MSGQ-GLSWEASQEE--AFLRSGAQFSPT-HGLALPQDGVYYLYCHVGYRGRTPPA-GRSRARSL     Mouse LyTβ
 57-  AHSTLKPAAHLIGDP----------------SKQNS-LLWRANTDR--AFLQDGFSLSN--NSLLVPTSGIYFVYSQVVFSGKAYSPKATSSPLYL     Human TNFβ
 54-  THGILKPAAHLVGYP----------------SKQNS-LLWRASTDR--AFLRHGFSLSN--NSLLIPTSGLYFVYSQVVFSGESCSPRAIPTPIYL     Mouse TNFβ
 82-  RTPSDKPVAHVVANP----------------QAEGQ-LQWLNRRAN--ALLANGVELRD--NQLVVPSEGLYLIYSQVLFKGQGCP----STHVLL     Human TNFα
 85-  QNSSDKPVAHVVANH----------------QVEEQ-LEWLSQRAN--ALLANGMDLKD--NQLVVPADGLYLVYSQVLFKGQGCP-----DYVLL     Mouse TNFα
```

FIG. 9B

```
      E         E/F loop         F            F/G loop            G             H       H/I loop       I
     -H-V---V--------YP----LLS---T--C-------------W--S-YLGGVF-L--GD-LYVNV---S---F-----TFFGLFKL             Consensus
08-  SHKVYMRNS------KYPQDLVMMEGKMMSYC--------TTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQ-TFFGLYKL      -281   Human FasL
06-  NHKVYMRNS------KYPEDLVLMEEKRLNYC--------TTGQIWAHSSYLGAVFNLTSADHLYVNISQLSLINFEESK-TFFGLYKL      -279   Mouse FasL
05-  SHKVYMRNF------KYPGDLVLMEEKKLNYC--------TTGQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESK-TFFGLYKL      -278   Rat FasL
90-  IASLCLKS-------PGRFERILLRAANTHSSAKPC---------GQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGF-TSFGLLKL      -261   Human CD40L
89-  IVGLWLKP-------SIGSERILLKAANTHSSSQLC---------EQQSVHLGGVFELQAGASVFVNVTEASQVIHRVGF-SSFGLLKL      -260   Mouse CD40L
12-  IQRKKVHV--------FGDELSLVTLFRCIQNMPETL-------P-NNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL     -285   Human AGP3
36-  IQRKKVHV--------FGDELSLVTLFRCIQNMPKTL-------P-NNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL     -309   Mouse AGP3
34-  YLQLMVYVVKTSI--KIPSSHNLMKGGSTKNWSGN-----SE--FHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDA-TYFGAFKVQDID  -316   Mouse OPGL
35-  YLQLMVYVTKTSI--KIPSSHTLMKGGSTKYWSGN-----SE--FHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDA-TYFGAFKVRDID  -317   Human OPGL
01-  K-NDKQMVQYIYKYTSYPDPILLMKSARNSCWSKD-----AE--YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA-SFFGAFLVG     -281   Human TRAIL
10-  KVRTKQLVQYIYKYTSYPDPIVLMKSARNSCWSRD-----AE--YGLYSIYQGGLFELKKNDRIFVSVTNEHLMDLDQEA-SFFGAFLIN     -291   Mouse TRAIL
59-  KLELLIN------------KHIKKQALVTVCESGMQTK--HVYQNLSQFLLDYLQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD     -234   Human CD30L
64-  TLQLLIN------------SKIKKQTLVTVCESGVQSK--NIYQNLSQFLLHYLQVNSTISVRVDNFQYVDTNTFPLDNVLSVFLYSSSD     -239   Mouse CD30L
58-  TLRSSLYRAGGA--YGPGTPELLLEGAETVTPVLDPARRQGYGPLWYTSVGFGGLVQLRRGERVYVNISHPDMVDFARGK-TFFGAVMVG     -244   Human LyTβ
23-  TLRSALYRAGGA--YGRGSPELLLEGAETVTPVVDPI---GYGSLWYTSVGFGGLAQLRSGERVYVNISHPDMVDYRRGK-TFFGAVMVG     -306   Mouse LyTβ
32-  AHEVQLFSS------QYPFHVPLLSSQKMVYP--------GLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPHLVLSPST-VFFGAFAL      -205   Human TNFβ
29-  AHEVQLFSS------QYPFHVPLLSAQKSVYP--------GLQGPWVRSMYQGAVFLLSKGDQLSTHTDGISHLHFSPSS-VFFGAFAL      -202   Mouse TNFβ
53-  THTISRIAV------SYQTKVNLLSAIKSPCQRETPEG--AEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL      -233   Human TNFα
55-  THTVSRFAI------SYQEKVNLLSAVKSPCPKDTPEG--AELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL      -235   Mouse TNFα
```

FIG. 10A

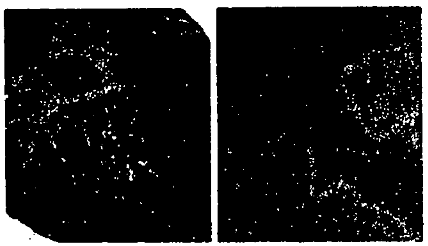


FIG. 10D

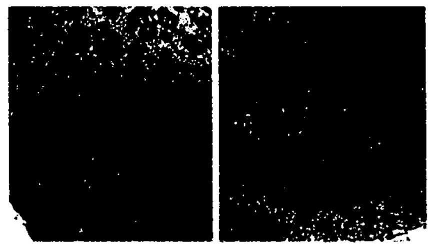


FIG. 10G

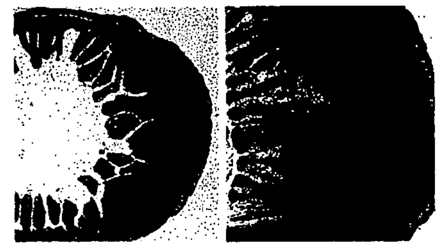


FIG. 10B

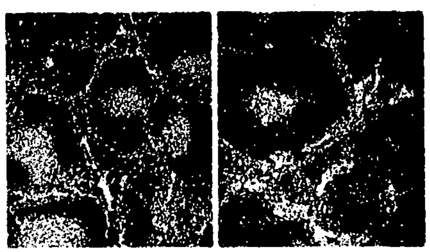


FIG. 10E

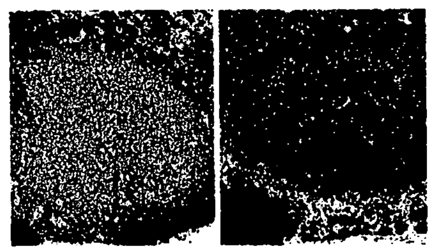


FIG. 10H

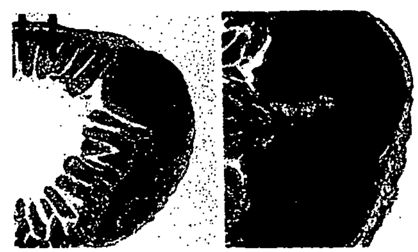


FIG. 10C

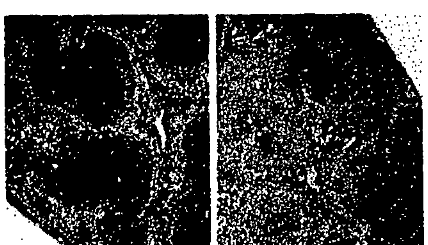


FIG. 10F

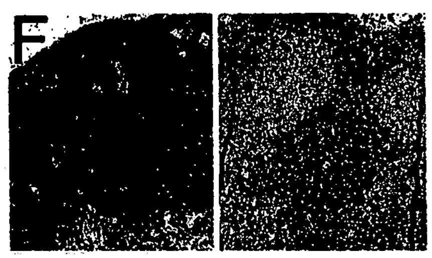


FIG. 10I

FIG. 11A

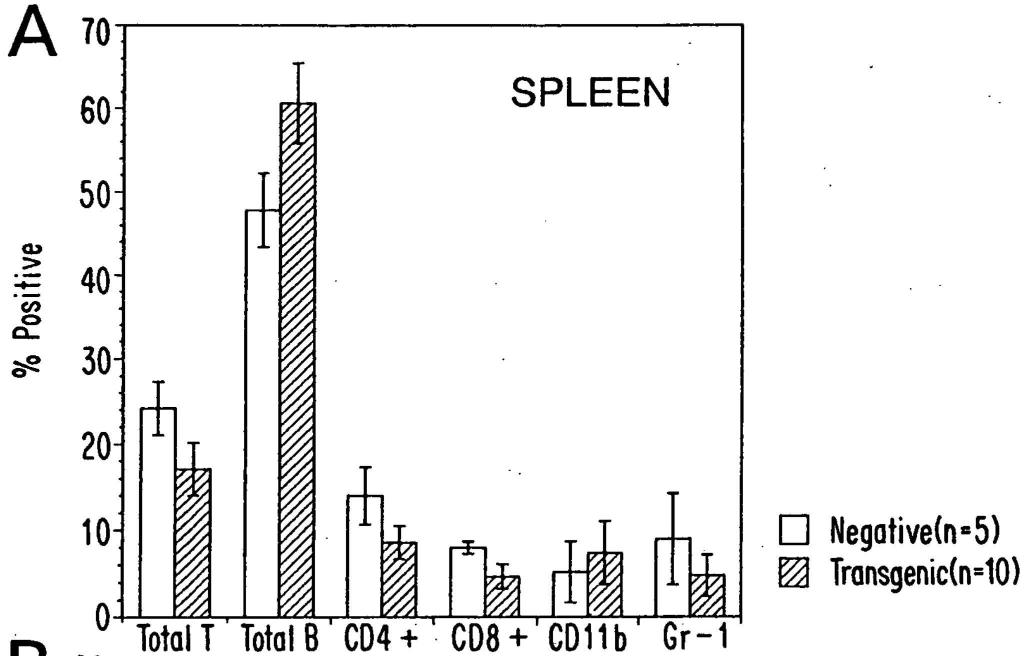


FIG. 11B

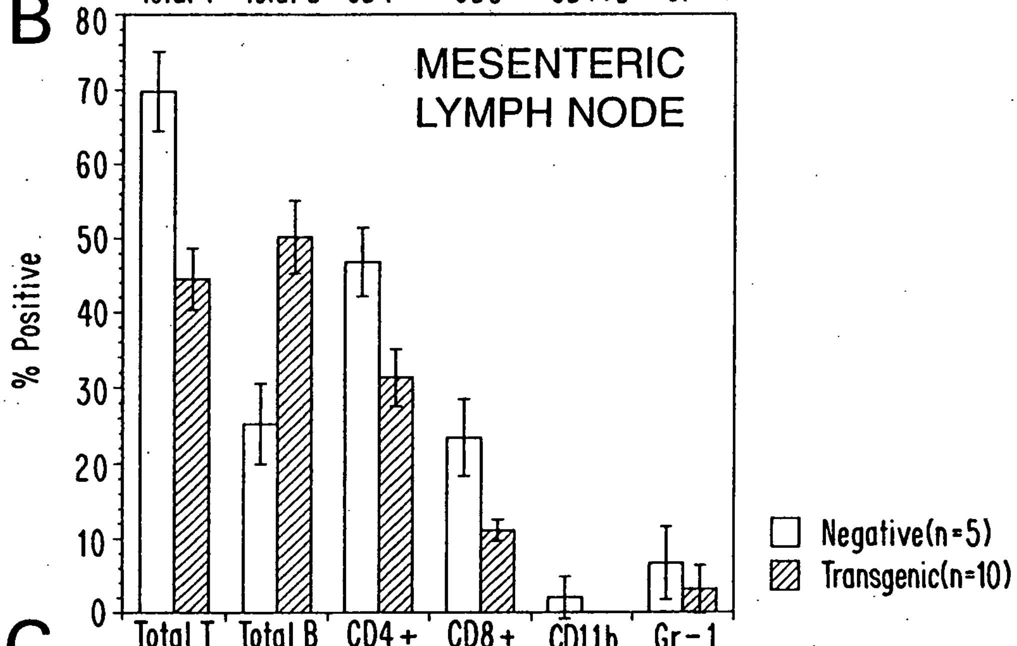


FIG. 11C

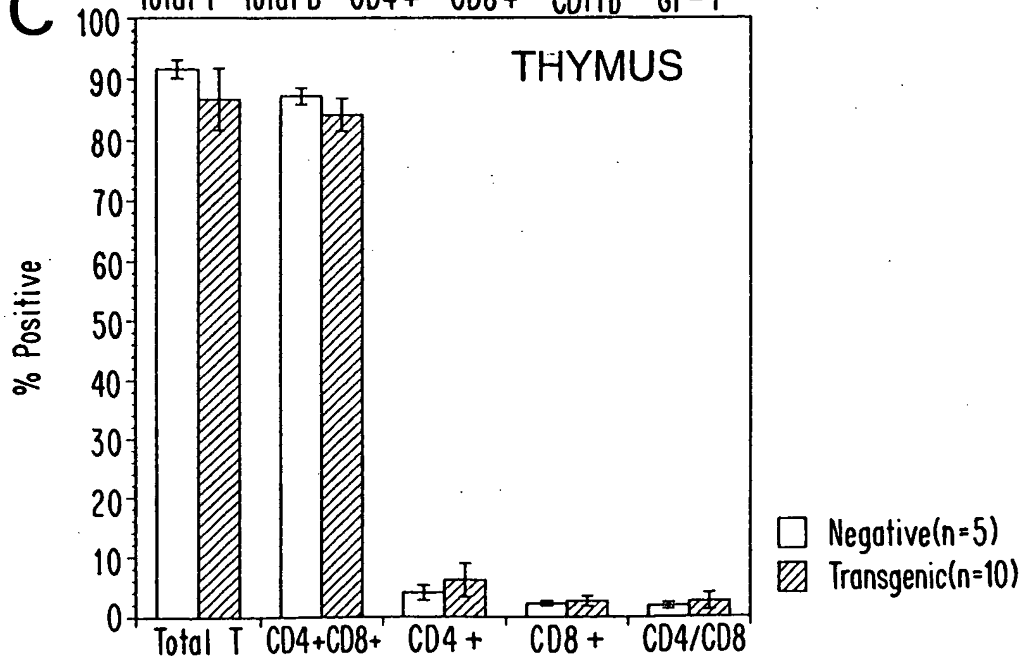


FIG. 12A

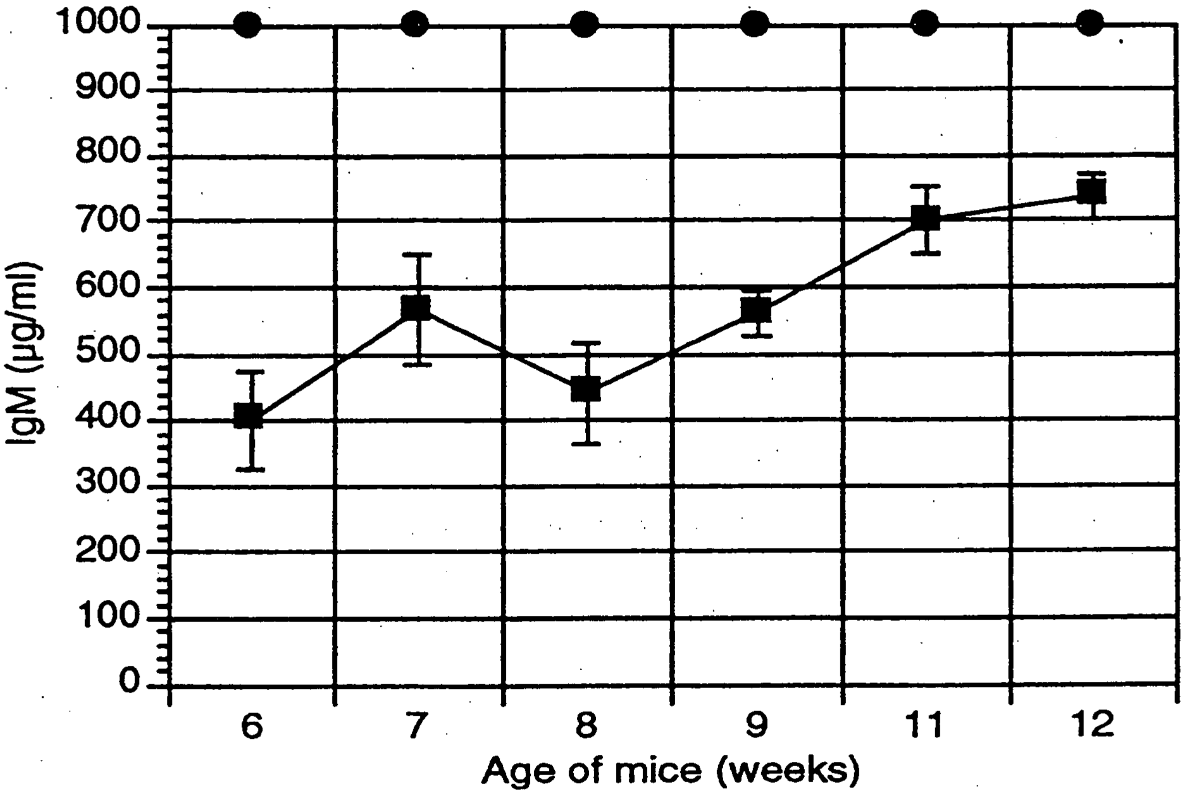


FIG. 12B

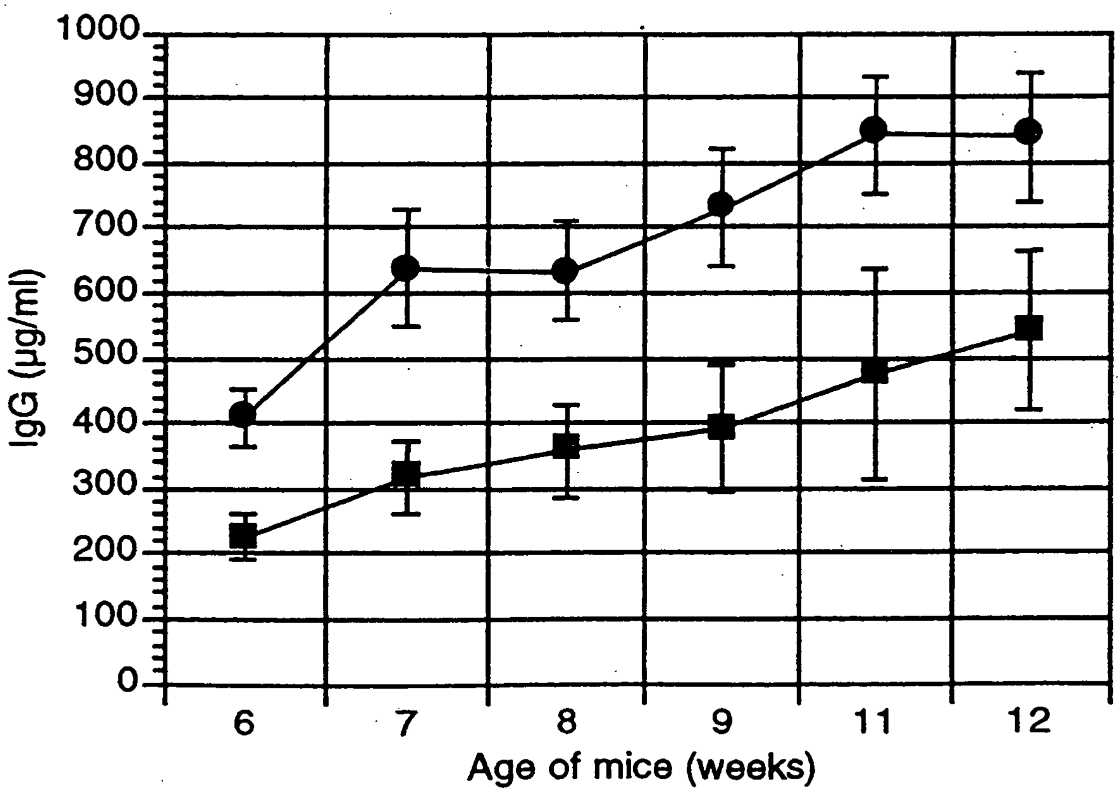


FIG. 12C

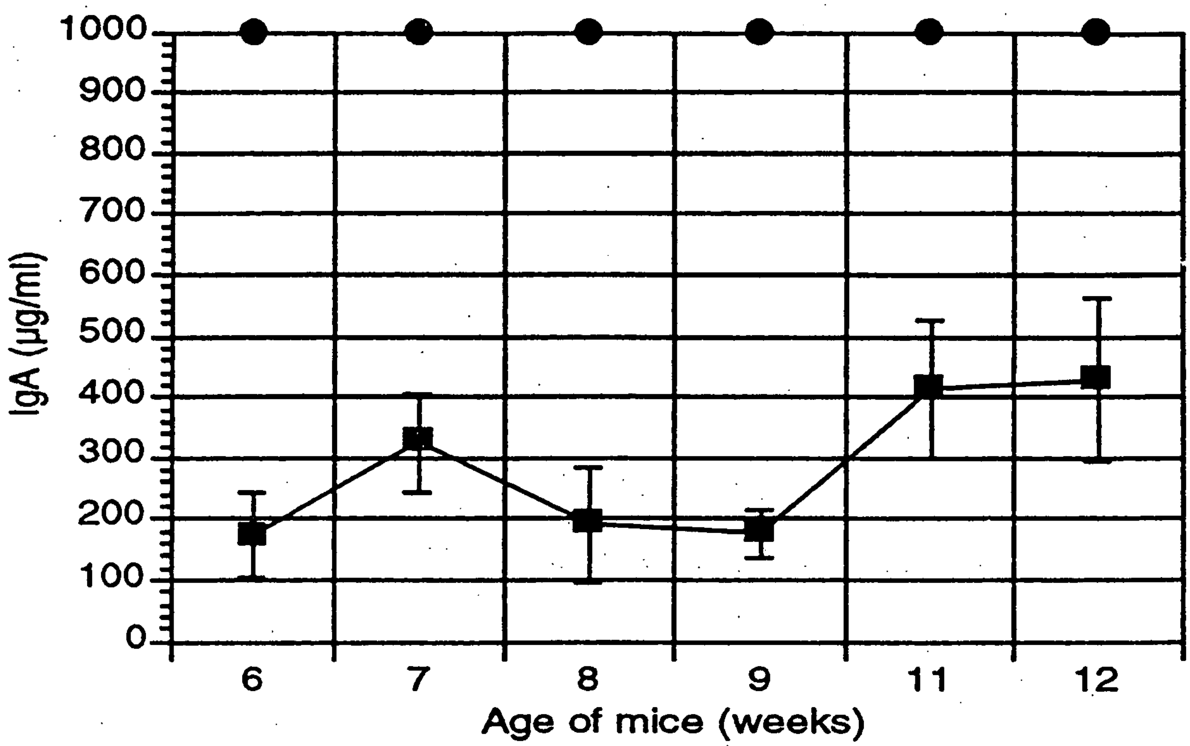


FIG. 12D

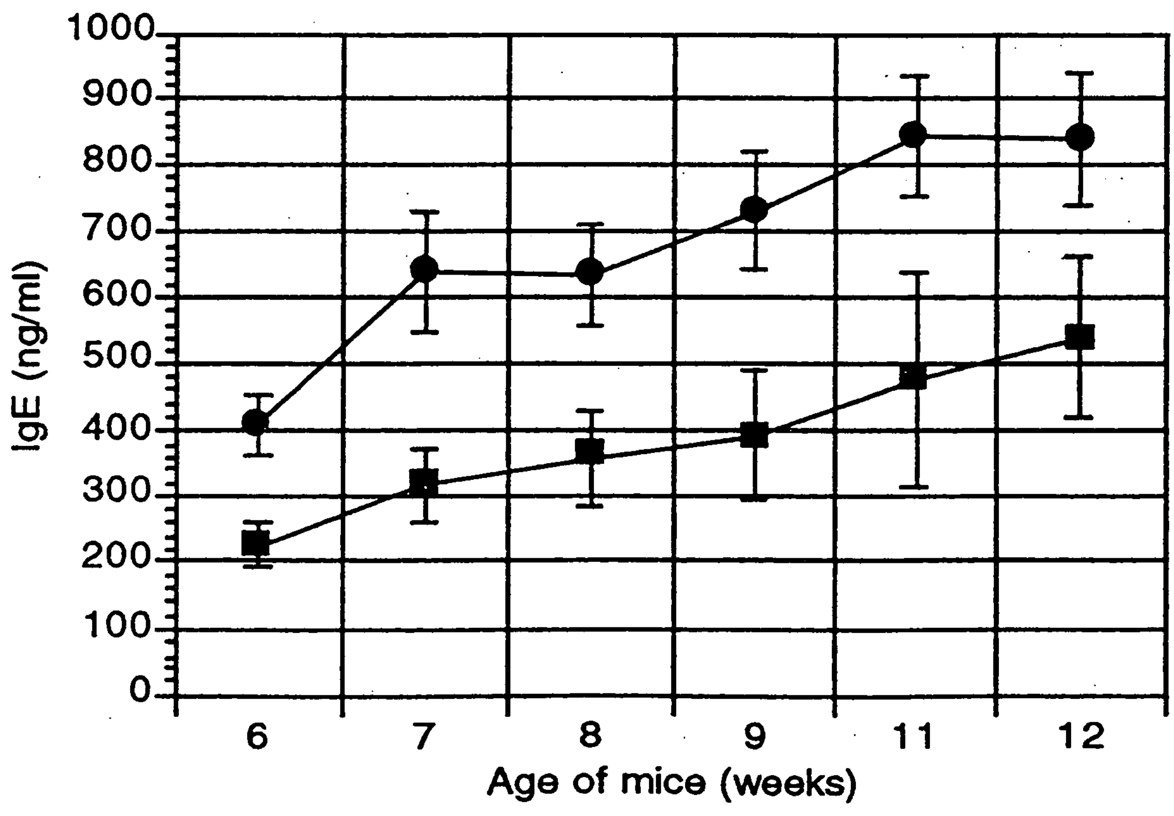


FIG. 13A

FIG. 13D

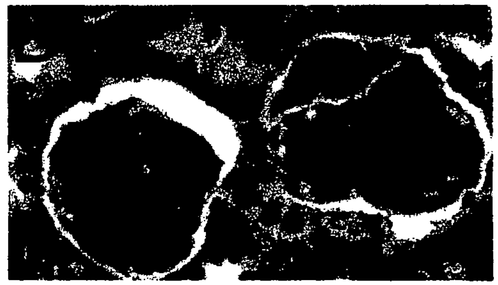


FIG. 13G

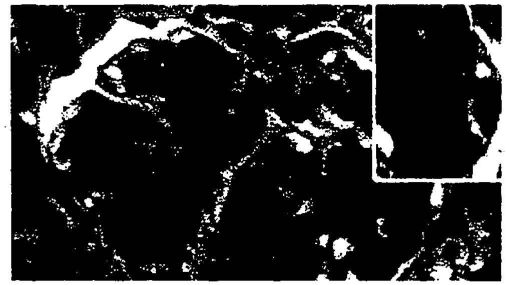


FIG. 13B

FIG. 13E

FIG. 13H

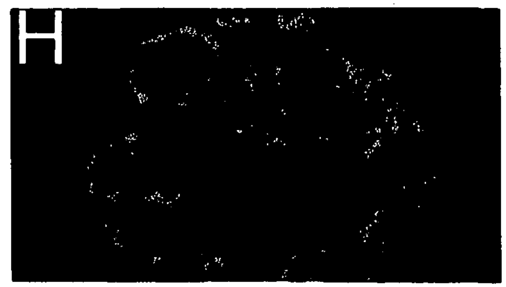


FIG. 13C

FIG. 13F

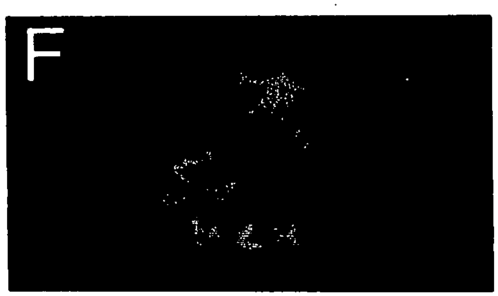


FIG. 13I

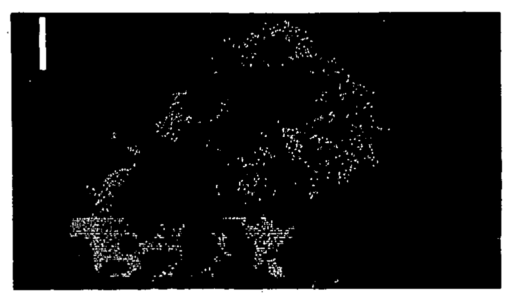


FIG. 14A

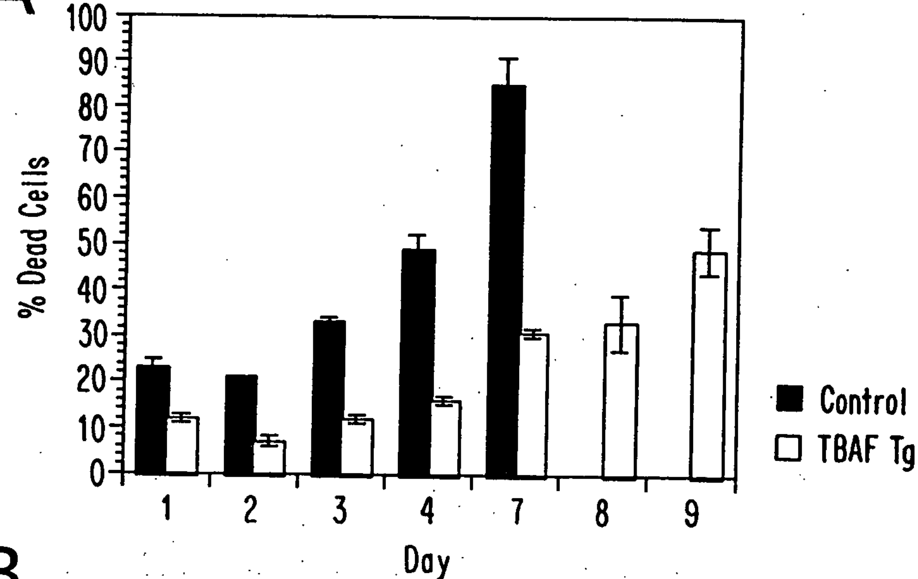


FIG. 14B

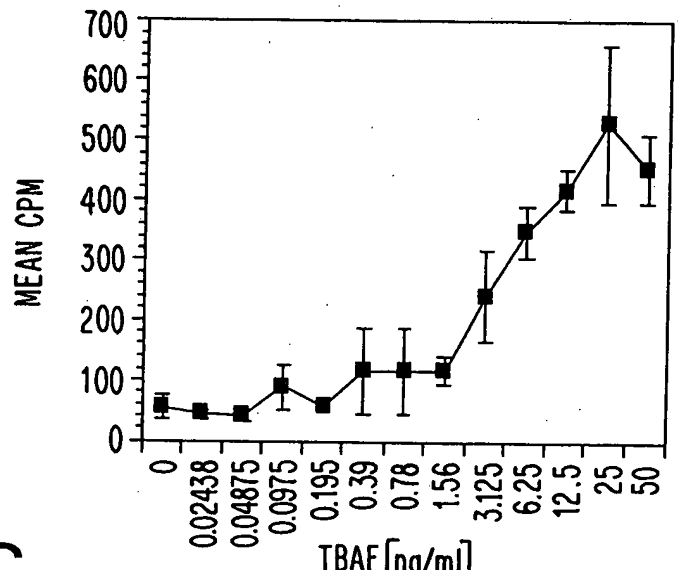


FIG. 14C

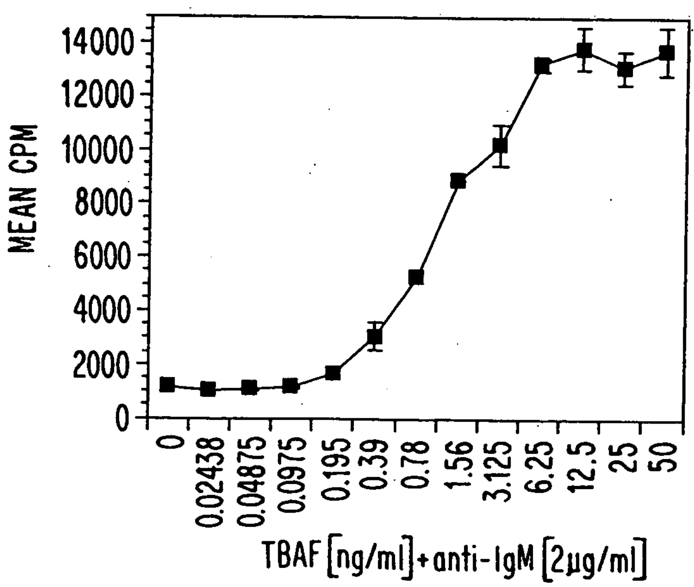


FIG. 15

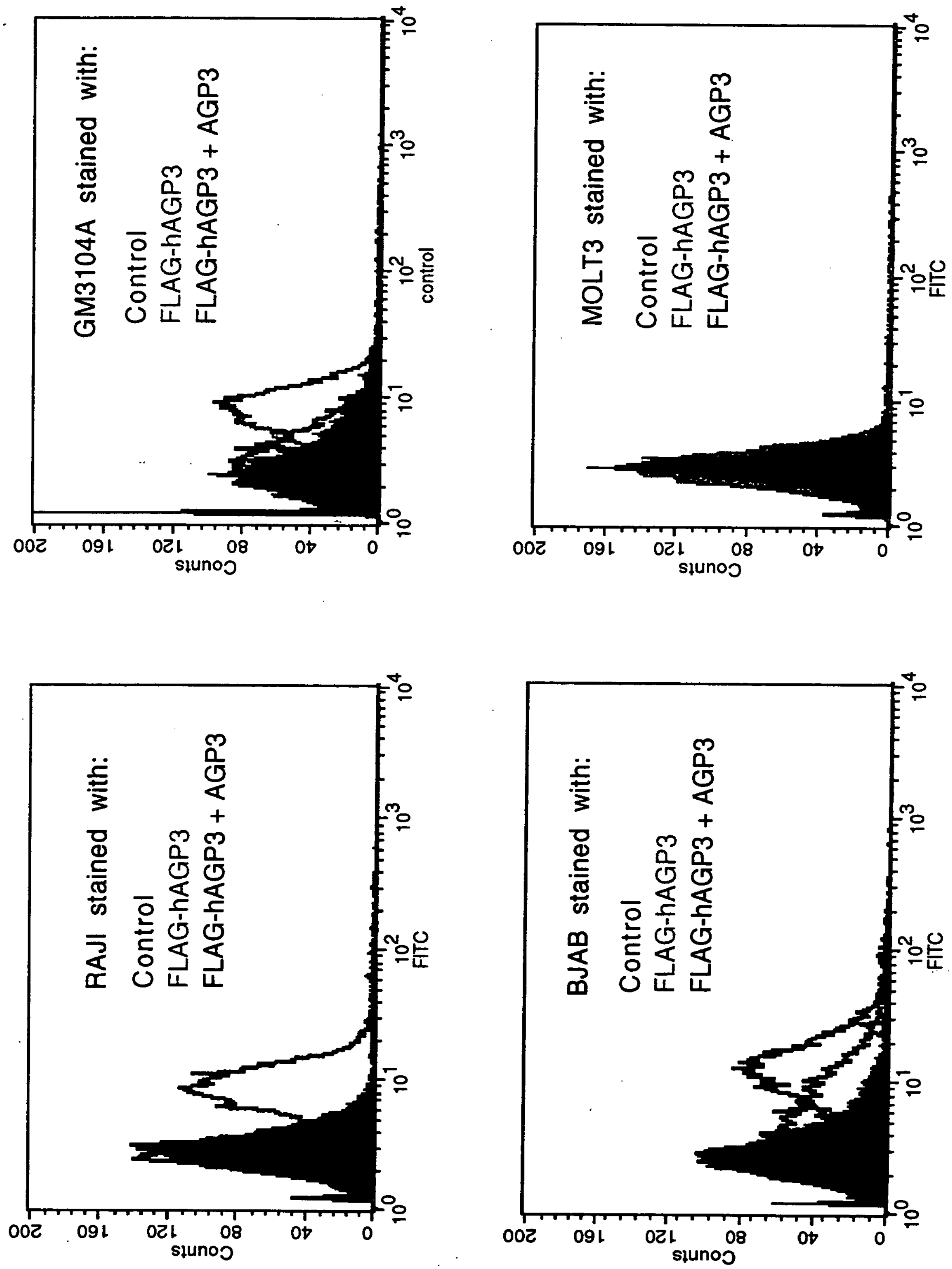

GM3104A stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
control
MOLT3 stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
FITC
RAJI stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
FITC
BJAB stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
FITC
0
40
80
120
160
200
10^0
10^1
10^2
10^3
10^4

FIG. 16

Alignment of AGP3-binding pools 13B4 and 13H11
N-terminal sequence

```
                .         .         .         .         .
  1 GTCGACCCACGCGTCCG.......ATCCTGAGTAATGAGTGGCCTGGGCC 43
    |||||||||||||||||       ||||||||||||||||||||||||||
  1 GTCGACCCACGCGTCCGAATAAGCATCCTGAGTAATGAGTGGCCTGGGCC 50
                .         .         .         .         .
 44 GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 93
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 100
                .         .         .         .         .
 94 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 143
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 150
                .         .         .         .         .
144 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTTGCAACC 193
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTTGCAACC 200
                .         .         .         .         .
194 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 243
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 250
                .         .         .         .         .
244 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 293
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 300
                .         .         .         .         .
294 TGCCTCCATCTGTGGACAGCACCCTAAGCAATGTGCATACTTCTGTGAGA 343
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 TGCCTCCATCTGTGGACAGCACCCTAAGCAATGTGCATACTTCTGTGAGA 350
                .         .         .         .         .
344 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 393
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 400
                .         .         .         .         .
```

FIG. 17

Human AGP3 receptor sequence

GTCGACCCACGCGTCCGATCCTGAGTAATGAGTGGCCTGGGCCGGAGCAGGCGAGGTGGC
M S G L G R S R R G G
CGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCACAGGGCCTGTGGACAGGGGTGGCTATG
R S R V D Q E E R F P Q G L W T G V A M
AGATCCTGCCCCGAAGAGCAGTACTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAA
R S C P E E Q Y W D P L L G T C M S C K
ACCATTTGCAACCATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGC
T I C N H Q S Q R T C A A F C R S L S C
CGCAAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTGTGCCTCC
R K E Q G K F Y D H L L R D C I S C A S
ATCTGTGGACAGCACCCTAAGCAATGTGCATACTTCTGTGAGAACAAGCTCAGGAGCCCA
I C G Q H P K Q C A Y F C E N K L R S P
GTGAACCTTCCACCAGAGCTCAGGAGACAGCGGAGTGGAGAAGTTGAAAACAATTCAGAC
V N L P P E L R R Q R S G E V E N N S D
AACTCGGGAAGGTACCAAGGACTGGAGCACAGAGGCTCAGAAGCAAGTCCAGCTCTCCCG
N S G R Y Q G L E H R G S E A S P A L P
GGGCTGAAGCTGAGTGCAGATCAGGTGGCCCTGGTCTACAGCACGCTGGGGCTCTGCCTG
G L K L S A D Q V A L V Y S T L G L C L
TGTGCCGTCCTCTGCTGCTTCCTGGTGGCGGTGGCCTGCTTCCTCAAGATGAGGGGGGAT
C A V L C C F L V A V A C F L K M R G D
CCCTGCTCCTGCCAGCCCCGCTCAAGGCCCCGTCAAAGTCCGGCCAAGTCTTCCCAGGAT
P C S C Q P R S R P R Q S P A K S S Q D
CACGCGATGGAAGCCGGCAGCCCTGTGAGCACATCCCCCGAGCCAGTGGAGACCTGCAGC
H A M E A G S P V S T S P E P V E T C S
TTCTGCTTCCCTGAGTGCAGGGCGCCCACGCAGGAGAGCGCAGTCACGCCTGGGACCCCC
F C F P E C R A P T Q E S A V T P G T P
GACCCCACTTGTGCTGGAAGGTGGGGGTGCCACACCAGGACCACAGTCCTGCAGCCTTGC
D P T C A G R W G C H T R T T V L Q P C
CCACACATCCCAGACAGCGGCCTTGGCATTGTGTGTGTGCCTGCCCAGGAGGGGGGCCCA
P H I P D S G L G I V C V P A Q E G G P
GGTGCATAAATGGGGGTCAGGGAGGGAAAGGAGGAGGGAGAGAGATGGAGAGGAGGGGAG
G A
AGAGAAAGAGAGGTGGGGAGAGGGGAGAGAGATATGAGGAGAGAGAGACAGAGGAGGCAG
AGAGGGAGAGAAACAGAGGAGACAGAGAGGGAGAGAGAGACAGAGGGAGAGAGAGACAGA
GAGGAAGAGAGGCAGAGAGGGAAAGAGGCAGAGAAGGAAAGAGACAGGCAGAGAAGGAGA
GAGGCAGAGAGGGAGAGAGGCAGAGAGGGAGAGAGGCAGAGAGACAGAGAGGGAGAGAGG
GACAGAGAGAGATAGAGCAGGAGGTCGGGGCACTCTGAGTCCCAGTTCCCAGTGCAGCTG
TAGGTCGTCATCACCTAACCACACGTGCAATAAAGTCCTCGTGCCTGCTGCTCACAGCCC
CCGAGAGCCCCTCCTCCTGG

FIG. 18

AGP3 receptor protein structure

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMR

SCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSL I

SCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENK II

LRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSE stalk
ASPALPGLKLSADQVAVYS

<u>TLGLCLCAVLCCFLVAVACFL</u> TM

KMRGDPCSCQPRSRPRQSPAKSSQDHAMEAGSPVSTSP IC
EPVETCSFCFPECRAPTQESAVTPGTPDTCAGRWGCHT
RTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

FIG. 19

Alignment of AGP3 receptor and TNFR1 extracellular domain

```
       10        20        30        40        50        60
LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTTCMSCKTICNHQS-QR    AGP3R
                              ||: :|  |  :: |  | | |:: :
VLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSIC--C-TKCHKGTYLYN   TNFR1
    20        30        40        50           60        70

       70           80        90       100       110
TCAAFCRSLSCRK-EQGKF-YDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPE    AGP3R
              | :  :: :||: |:|:|   :: || |:|| | | ::  |
DCPGPGQDTDCRECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRK   TNFR1
        80        90       100        110       120
```

FIG. 20

Human AGP3 receptor mRNA tissue distribution

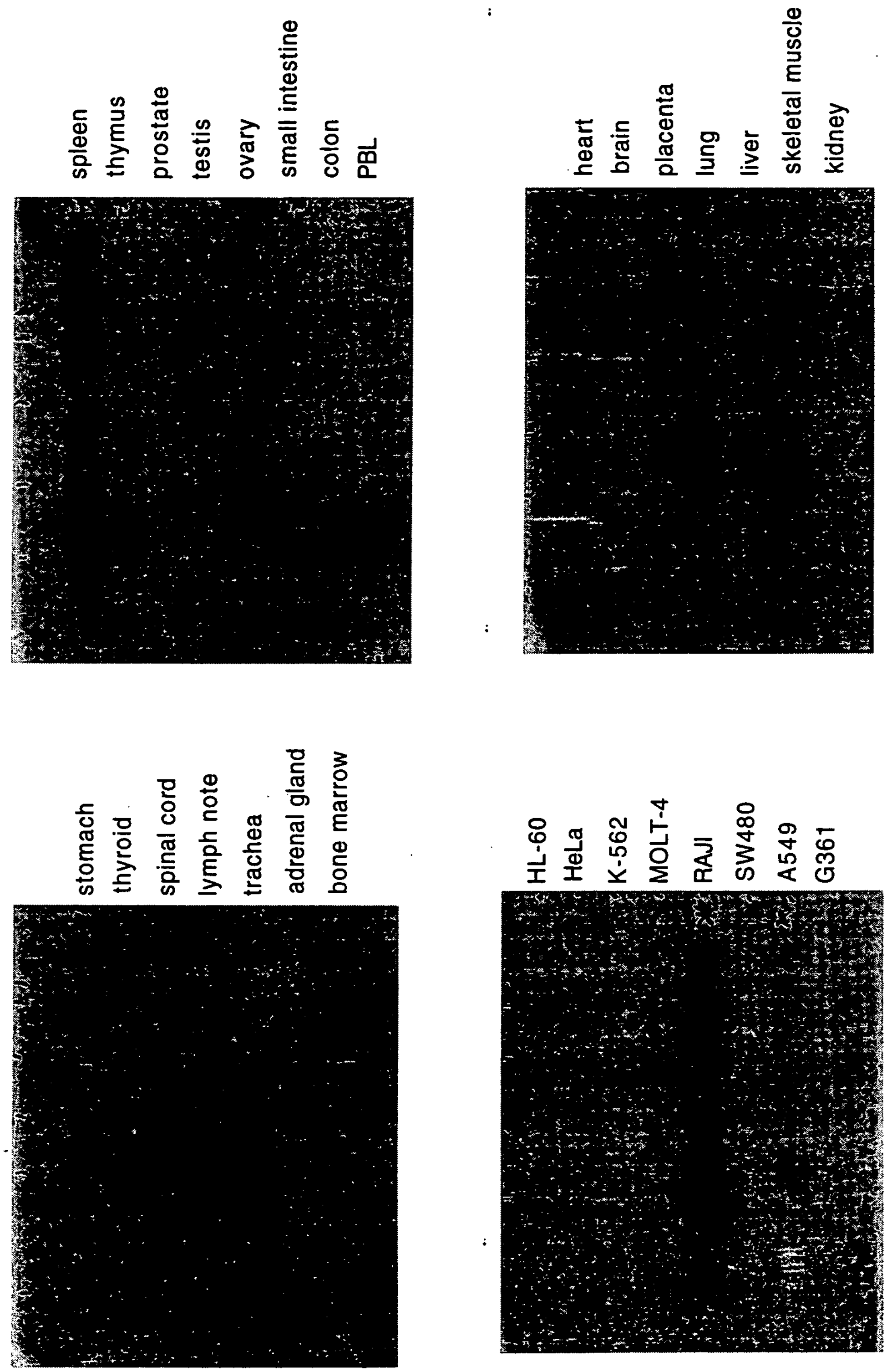
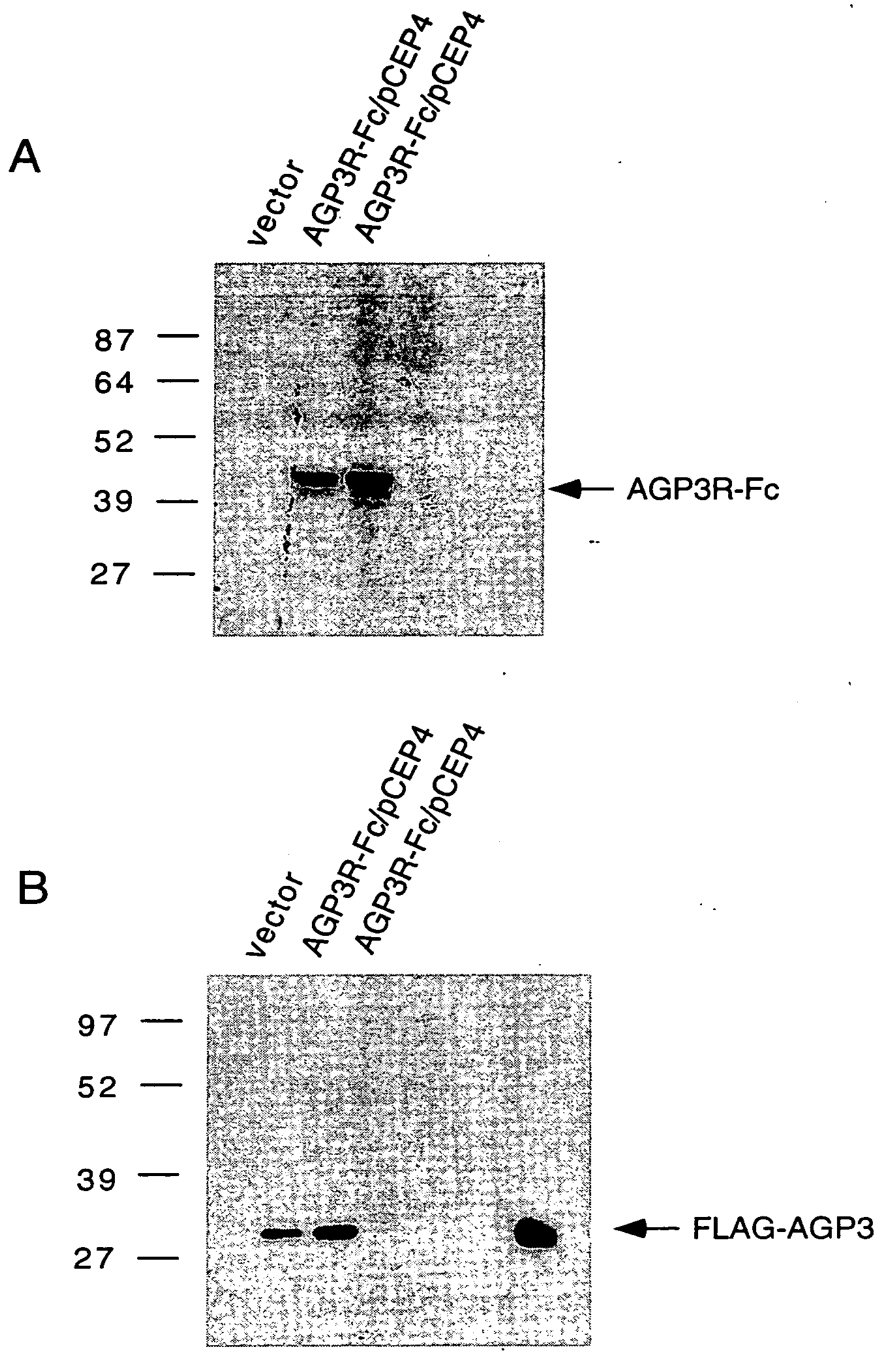


FIG 21


A
vector
AGP3R-Fc/pCEP4
AGP3R-Fc/pCEP4
87
64
52
39
27
AGP3R-Fc
B
vector
AGP3R-Fc/pCEP4
AGP3R-Fc/pCEP4
97
52
39
27
FLAG-AGP3